

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Agonist antibody

<130> FP1009

<141> 2001-04-17

<150> JP2000-115246

<151> 2000-04-17

<150> JP2000-321821

<151> 2000-10-20

<150> JP2000-321822

<151> 2000-10-20

<150> PCT/JP01/01912

<151> 2001-03-12

<160> 109

<210> 1

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

ccatcctaatacgcactcact atagggc 27

<210> 2

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 2

ggatcccggg tggatggtgg gaagatg 27

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 3

ggatcccggg ccagtggata gacagatg 28

<210> 4

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 4

ggatcccggg agtggataga ccgatg 26

<210> 5

<211> 394

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(393)

<223> pGEM-M1L. 1-57;signal peptide, 58-394;mature peptide

<400> 5

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct 45

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro

5 10 15

gcg tcc agc agt gat gtt gtg atg acc caa act cca ctc tcc ctg 90

Ala Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu

20 25 30

cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt 135

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser

35 40 45

cag agc ctt cta cac agt aaa gga aac acc tat tta caa tgg tac 180

Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr

50 55 60

cta cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt 225

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val

65 70 75

tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 270

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

80 85 90

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 315

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu

95 100 105

gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 360

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

110 115 120

acg tcc gga ggg ggg acc aag ctg gaa ata aaa c 394

Thr Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys

125 130

<210> 6

<211> 409

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(408)

<223> pGEM-M1H. 1-57;signal peptide, 58-409;mature peptide

<400> 6

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca 45

Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala

5 10 15

ggt gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg 90

Gly Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu

10 25 30

gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly

35 40 45

tac acc ttc gtt aac cat gtt atg cac tgg gtg aag cag aag cca 180

Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro

50 55 60

ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

65 70 75

ggt act aag tac aat gag aag ttc aag ggc aag gcc aca ctg act 270

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

80 85 90

tca gag aaa tcc tcc agc gca gcc tac atg gag ctc agc agc ctg 315

Ser Glu Lys Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu

95 100 105

gcc tct gag gac tct gcg gtc tac tac tgt gca aga ggg ggt tac 360

Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr

110 115 120

tat agt tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405

Tyr Ser Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

125 130 135

tca g 409

Ser

<210> 7

<211> 394

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(393)

<223> pGEM-M2L. 1-57;signal peptide, 58-394;mature peptide

<400> 7

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct 45

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro

5 10 15

ggt tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg 90
 Gly Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu
 20 25 30
 cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt 135
 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
 35 40 45
 cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac 180
 Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr
 50 55 60
 ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt 225
 Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 65 70 75
 tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 270
 Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 80 85 90
 tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct gag 315
 Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu
 95 100 105
 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 360
 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
 110 115 120
 acg ttc gga ggg ggg acc aag ctg gaa ata aaa c 394
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 125 130

<210> 8
 <211> 409
 <212> DNA
 <213> Mus
 <220>
 <221> CDS
 <222> (1)...(408)
 <223> pGEM-M2H. 1-57;signal peptide, 58-409;mature peptide
 <400> 8

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca 45
 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala
 5 10 15
 ggt gtc cac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg 90
 Gly Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
 20 25 30
 gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135
 Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
 35 40 45
 tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca 180
 Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro
 50 55 60
 ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp
 65 70 75
 ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act 270
 Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr
 80 85 90
 tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg 315
 Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu
 95 100 105
 gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt tac 360
 Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr
 110 115 120
 tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405
 Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 125 130 135
 tca g 409
 Ser

<210> 9
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 9
 cccaagcttc caccatgaag ttgcctgtta gg 32

<210> 10
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 10
 cccaagcttc caccatggaa tggagctgga ta 32

<210> 11
 <211> 34
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 11
 cgcggaatcca ctcacgtttt atttcagct tggt 34

<210> 12
 <211> 34
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 12

cgcggatcca ctcacctgag gagactgtga gagt 34

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 13

catgcatgg cgcaggtcca gctgcagcag 30

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 14

accaccacct gaggagactg tgagagt 27

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 15

gtctcctcag gtggtggtgg ttcgggt 27

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 16

cacaacatcc gatccgccac caccoga 27

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 17

ggcggatcgg atgtgtgat gacccaa 27

<210> 18

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 18

ccggaattct cattattat cgtcatcgtc ttgtagtct ttatttcca gcttgg 57

<210> 19

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence and nucleotide sequence

<400> 19

ggg ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt ggc gga tgc 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

5

10

15

<210> 20

<211> 828

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(826)

<223> pscM1. MABL1-scFv

<400> 20

atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc 45

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu

5

10

15

gct gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga 90

Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly

20

25

30

cct gac ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag 135

Pro Asp Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys

35

40

45

gct tct gga tac acc ttc gtt aac cat gtt atg cac tgg gtg aag 180

Ala Ser Gly Tyr Thr Phe Val Asn His Val Met His Trp Val Lys

50

55

60

cag aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct 225

Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro

```

      65      70      75
tac aat gat ggt act aag tac aat gag aag ttc aag ggc aag gcc 270
Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala
      80      85      90
aca ctg act tca gag aaa tcc tcc agc gca gcc tac atg gag ctc 315
Thr Leu Thr Ser Glu Lys Ser Ser Ser Ala Ala Tyr Met Glu Leu
      95     100     105
agc agc ctg gcc tct gag gac tct gcg gtc tac tac tgt gca aga 360
Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
     110     115     120
ggg ggt tac tat agt tac gac gac tgg ggc caa ggc acc act ctc 405
Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu
     125     130     135
aca gtc tcc tca ggt ggt ggt ggt tgc ggt ggt ggt tgc ggt 450
Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
     140     145     150
ggt ggc gga tgc gat gtt gtg atg acc caa act cca ctc tcc ctg 495
Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
     155     160     165
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt 540
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
     170     175     180
cag agc ctt cta cac agt aaa gga aac acc tat tta caa tgg tac 585
Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr
     185     190     195
cta cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt 630
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
     200     205     210
tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 675
Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
     215     220     225
tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 720
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
     230     235     240
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 765
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
     245     250     255
acg tcc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac 810
Thr Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp
     260     265     270
gat gac gat aaa taa tga 828
Asp Asp Asp Lys

```

<210> 21

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 21

acgcgtcgac tcccaggtcc agctgcagca g 31

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 22

gaaggtgtat ccagaagc 18

<210> 23

<211> 819

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(813)

<223> pCHOM1. MABL1-scFv

<400> 23

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca 45

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr

5 10 15

ggt gtc gac tcc cag gtc cag ctg cag cag tct gga cct gac ctg 90

Gly Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu

20 25 30

gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly

35 40 45

tac acc ttc gtt aac cat gtt atg cac tgg gtg aag cag aag cca 180

Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro

50 55 60

ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

65 70 75

ggt act aag tac aat gag aag ttc aag ggc aag gcc aca ctg act 270

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

80 85 90

tca gag aaa tcc tcc agc gca gcc tac atg gag ctc agc agc ctg 315

Ser Glu Lys Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu

95 100 105

gcc tct gag gac tct gcg gtc tac tac tgt gca aga ggg ggt tac 360

Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr

110 115 120

tat agt tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405
 Tyr Ser Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 125 130 135
 tca ggt ggt ggt ggt tgc ggt ggt ggt tgc ggt ggt ggc gga 450
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 140 145 150
 tcg gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc agt 495
 Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
 155 160 165
 ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt 540
 Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 170 175 180
 cta cac agt aaa gga aac acc tat tta caa tgg tac cta cag aag 585
 Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys
 185 190 195
 cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga 630
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 200 205 210
 TTT TCT GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGG ACA 675
 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
 215 220 225
 gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga 720
 Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
 230 235 240
 gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg tcc gga 765
 Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly
 245 250 255
 ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 810
 Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp
 260 265 270
 aaa taa tga 819
 Lys

<210> 24

<211> 828

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(822)

<223> pscM2. MABL2-scFv

<400> 24

atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc 45
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu
 5 10 15
 gct gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga 90
 Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly

20 25 30
 cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag 135
 Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 35 40 45
 gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag 180
 Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys
 50 55 60
 cag aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct 225
 Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro
 65 70 75
 tac aat gat ggt act aag tat aat gag aag ttc aag gac aag gcc 270
 Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala
 80 85 90
 act ctg act tca gac aaa tcc tcc acc aca gcc tac atg gac ctc 315
 Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu
 95 100 105
 agc agc ctg gcc tct gag gac tct gcg gtc tat tac tgt gca aga 360
 Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
 110 115 120
 ggg ggt tac tat act tac gac gac tgg ggc caa ggc acc act ctc 405
 Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu
 125 130 135
 aca gtc tcc tca ggt ggt ggt ggt tgg ggt ggt ggt tgg ggt 450
 Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 140 145 150
 ggt ggc gga tgg gat gtt gtg atg acc caa agt cca ctc tcc ctg 495
 Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu
 155 160 165
 cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt 540
 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
 170 175 180
 cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac 585
 Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr
 185 190 195
 ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt 630
 Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 200 205 210
 tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 675
 Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 215 220 225
 tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct gag 720
 Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu
 230 235 240
 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 765
 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
 245 250 255
 acg ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac 810

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp
 260 265 270

gat gac gat aaa taa tga 828

Asp Asp Asp Lys

<210> 25

<211> 819

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(813)

<223> pCHOM2. MABL2-scFv

<400> 25

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca 45

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr

5 10 15

ggt gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg 90

Gly Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu

20 25 30

gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly

35 40 45

tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca 180

Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro

50 55 60

ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

65 70 75

ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act 270

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

80 85 90

tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg 315

Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu

95 100 105

gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt tac 360

Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr

110 115 120

tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405

Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

125 130 135

tca ggt ggt ggt ggt tgg ggt ggt ggt tgg ggt ggt ggc gga 450

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

140 145 150

tgg gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt 495

Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser

155 160 165

ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt 540
 Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 170 175 180
 gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag 585
 Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys
 185 190 195
 cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga 630
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 200 205 210
 ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca 675
 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr
 215 220 225
 gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga 720
 Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
 230 235 240
 gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga 765
 Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
 245 250 255
 ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 810
 Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp
 260 265 270
 aaa taa tga 819
 Lys

<210> 26
 <211> 456
 <212> DNA
 <213> Mus
 <220>
 <221> CDS
 <222> (1)...(450)
 <223> pCHO-shIAP. Soluble human IAP
 <400> 26

atg tgg ccc ctg gta gcg gcg ctg ttg ctg ggc tcg gcg tgc tgc 45
 Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys
 5 10 15
 gga tca gct cag cta cta ttt aat aaa aca aaa tct gta gaa ttc 90
 Gly Ser Ala Gln Leu Leu Phe Asn Lys Thr Lys Ser Val Glu Phe
 20 25 30
 acg ttt tgt aat gac act gtc gtc att cca tgc ttt gtt act aat 135
 Thr Phe Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn
 35 40 45
 atg gag gca caa aac act act gaa gta tac gta aag tgg aaa ttt 180
 Met Glu Ala Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe
 50 55 60
 aaa gga aga gat att tac acc ttt gat gga gct cta aac aag tcc 225
 Lys Gly Arg Asp Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser

65 70 75
 act gtc ccc act gac ttt agt agt gca aaa att gaa gtc tca caa 270
 Thr Val Pro Thr Asp Phe Ser Ser Ala Lys Ile Glu Val Ser Gln
 80 85 90
 tta cta aaa gga gat gcc tct ttg aag atg gat aag agt gat gct 315
 Leu Leu Lys Gly Asp Ala Ser Leu Lys Met Asp Lys Ser Asp Ala
 95 100 105
 gtc tca cac aca gga aac tac act tgt gaa gta aca gaa tta acc 360
 Val Ser His Thr Gly Asn Tyr Thr Cys Glu Val Thr Glu Leu Thr
 110 115 120
 aga gaa ggt gaa acg atc atc gag cta aaa tat cgt gtt gtt tca 405
 Arg Glu Gly Glu Thr Ile Ile Glu Leu Lys Tyr Arg Val Val Ser
 125 130 135
 tgg ttt tct cca aat gaa aat gac tac aag gac gac gat gac aag 450
 Trp Phe Ser Pro Asn Glu Asn Asp Tyr Lys Asp Asp Asp Asp Lys
 140 145 150
 tga tag 456

<210> 27
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 27
 ggaattccat atgcaagtgc aacttcaaca gtctggacct gaactg 46

<210> 28
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> PCR primer
 <400> 28
 ggaattctca ttattttatt tccagcttgg t 31

<210> 29
 <211> 741
 <212> DNA
 <213> Mus
 <220>
 <221> CDS
 <222> (1)...(735)
 <223> pscM2DEm02. MABL2-scFv
 <400> 29
 atg caa gtg caa ctt caa cag tct gga cct gaa ctg gta aag cct 45
 Met Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro

5	10	15	
ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc	90		
Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
20	25	30	
gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc	135		
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly			
35	40	45	
ctt gag tgg att gga tat att tat cct tac aat gat ggt act aag	180		
Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys			
50	55	60	
tat aat gag aag ttc aag gac aag gcc act ctg act tca gac aaa	225		
Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys			
65	70	75	
tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag	270		
Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu			
80	85	90	
gac tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac	315		
Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr			
95	100	105	
gac gac tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt	360		
Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly			
110	115	120	
ggg ggt tgc ggt ggt ggt ggt tgc ggt ggt ggc gga tgc gat gtt	405		
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val			
125	130	135	
gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat	450		
Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp			
140	145	150	
caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt	495		
Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser			
155	160	165	
aat gga aag acc tat tta cat tgg tac ctg cag aag cca ggc cag	540		
Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln			
170	175	180	
tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg	585		
Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly			
185	190	195	
gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca	630		
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr			
200	205	210	
ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc	675		
Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe			
215	220	225	
tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc	720		
Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr			
230	235	240	
aag ctg gaa ata aaa taa tga	741		

Lys Leu Glu Ile Lys

<210> 30

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 30

cagacagtgg ttcaaagt 18

<210> 31

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 31

cgcgctcgacc gatccgccac caccggaacc accaccaccc gaaccaccac cacctttat 60
ttcagcttg gt 72

<210> 32

<211> 1605

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(1599)

<223> pCHOM2(Fv)2. MABL2-sc(Fv)2

<400> 32

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca 45

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr

5 10 15

ggt gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg 90

Gly Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu

20 25 30

gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly

35 40 45

tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca 180

Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro

50 55 60

ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

65 70 75

ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act 270

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

80	85	90	
tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg	315		
Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu			
95	100	105	
gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt tac	360		
Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr			
110	115	120	
tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc	405		
Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser			
125	130	135	
tca ggt ggt ggt ggt tcc ggt ggt ggt ggt tcc ggt ggt ggc gga	450		
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly			
140	145	150	
tcg gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt	495		
Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser			
155	160	165	
ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt	540		
Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu			
170	175	180	
gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag	585		
Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys			
185	190	195	
cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga	630		
Pro Gly Gln Ser Pro Lys Leu Ile Tyr Lys Val Ser Asn Arg			
200	205	210	
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca	675		
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr			
215	220	225	
gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga	720		
Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly			
230	235	240	
ggt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga	765		
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly			
245	250	255	
ggg ggg acc aag ctg gaa ata aaa ggt ggt ggt ggt tcc ggt ggt	810		
Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly			
260	265	270	
ggt ggt tcc ggt ggt ggc gga tcc gtc gac tcc cag gtc cag ctg	855		
Gly Gly Ser Gly Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu			
275	280	285	
cag cag tct gga cct gaa ctg gta aag cct ggg gct tca gtg aag	900		
Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys			
290	295	300	
atg tcc tgc aag gct tct gga tac acc ttc gct aac cat gtt att	945		
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile			
305	310	315	
cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg att gga	990		

His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly
 320 325 330
 tat att tat cct tac aat gat ggt act aag tat aat gag aag ttc 1035
 Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
 335 340 345
 aag gac aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc 1080
 Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala
 350 355 360
 tac atg gac ctg agc agc ctg gcc tct gag gac tct gcg gtc tat 1125
 Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr
 365 370 375
 tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 1170
 Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln
 380 385 390
 ggc acc act ctg aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt 1215
 Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 395 400 405
 ggt ggt tcg ggt ggt ggc gga tcg gat gtt gtg atg acc caa agt 1260
 Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
 410 415 420
 cca ctg tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 1305
 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 425 430 435
 tgc aga tca agt cag agc ctt gtg cac agt aat gga aag acc tat 1350
 Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr
 440 445 450
 tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctg ctg 1395
 Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu
 455 460 465
 atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc 1440
 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
 470 475 480
 agt ggc agt gga tca gtg aca gat ttc aca ctg atg atc agc aga 1485
 Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg
 485 490 495
 gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca 1530
 Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr
 500 505 510
 cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 1575
 His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 515 520 525
 gac tac aaa gac gat gac gat aaa taa tga 1605
 Asp Tyr Lys Asp Asp Asp Asp Lys
 530

<210> 33

<211> 23

<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 33
tgaggaattc ccaccatggg atg 23

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 34
cacgacgtca ctcgagactg tgagagtggg gccttgcccc 40

<210> 35
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 35
agtctcgagt gacgtcgtga tgacccaaag tccactctcc 40

<210> 36
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 36
gactggatcc tcattattta tcgtcatcgt c 31

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer
<400> 37
cgcgtaatac gactcactat ag 22

<210> 38
<211> 46
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 38

gcaattggac ctgtttatc tcgagcttg tccccctcc gaacgt 46

<210> 39

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 39

gtctgagata aaacaggacc aattgcagca gtctggacct gaact 45

<210> 40

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 40

gactggatcc tcattattta tcgtcatcgt cttgtagtc tgaggagact gtgagagtgg 60

<210> 41

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 41

gactgaattc ccaccatgaa gttgcctgtt ag 32

<210> 42

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 42

cagtctcgag tgggtgttcc gacgtcgtga tgacccaaag 40

<210> 43

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 43

cagtctcgag tgggtggtggt tccgacgtcg tgatgacca aag 43

<210> 44

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 44

cagtctcgag tgggtggtggt ggtccgacg tcgtgatgac ccaaag 46

<210> 45

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 45

cagtctcgag tgggtggtggt ggtggtccg acgtcgtgat gacccaaag 49

<210> 46

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 46

cagtctcgag tgggtggtggt ggtggtggt cgcacgtcgt gatgacccaa ag 52

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 47

ggccgcacgtg tgcacgaat 20

<210> 48

<211> 780

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(768)

<223> CF2HL-0/pCOS1. MABL2-scFv<HL-0>

<400> 48

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt gtc 51

MET Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val

5 10 15

gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag cct ggg 102

Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly

20 25 30

gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc gct aac cat 153

Ala Ser Val Lys MET Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn His

35 40 45 50

gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg att gga 204

Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly

55 60 65

tat att tat cct tac aat gat ggt act aag tat aat gag aag ttc aag gac 255

Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp

70 75 80 85

aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc tac atg gac ctc 306

Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu

90 95 100

agc agc ctg gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt 357

Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly

105 110 115

tac tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcg agt 408

Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser

120 125 130 135

gac gtc gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat 459

Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp

140 145 150

caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt aat gga 510

Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly

155 160 165 170

aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc 561

Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu

175 180 185

ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt 612

Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser

190 195 200

ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct 663

Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val Glu Ala

205 210 215 220

gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 714

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr

225 230 235

ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 765

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp

240 245 250 255

aaa taa tga gga tcc 780

Lys

<210> 49

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 49

caagctcgag ataaaatccg gaggccaggt ccaattgcag cagtc 45

<210> 50

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 50

caagctcgag ataaaatccg gaggtggcca ggtccaattg cagcagtc 48

<210> 51

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 51

caagctcgag ataaaatccg gaggtggtgg ccagggtcaa ttgcagcagt c 51

<210> 52

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 52

caagctcgag ataaaatccg gaggtggtgg tggccagggtc caattgcagc agtc 54

<210> 53

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 53

caagctcgag ataaaatccg gaggtggtgg tggggccag gtccaattgc agcagtc 57

<210> 54

<211> 780

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(768)

<223> CF2LH-0/pCOS1. MABL2-scFv<LH-0>

<400> 54

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct ggt tcc 51

MET Lys Leu Pro Val Arg Leu Leu Val Leu MET Phe Trp Ile Pro Gly Ser

5 10 15

agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt 102

Ser Ser Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu

20 25 30

gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt 153

Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser

35 40 45 50

aat gga aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca 204

Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro

55 60 65

aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg 255

Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg

70 75 80 85

ttc agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg 306

Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val

90 95 100

gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg 357

Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro

105 110 115

tac acg ttc gga ggg ggg acc aag ctc gag ata aaa cag gtc caa ttg cag 408

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gln Val Gln Leu Gln

120 125 130 135

cag tct gga cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc 459

Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys MET Ser Cys

140 145 150

aag gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag cag 510

Lys Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln

155 160 165 170

aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 561

Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

175 180 185

ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act tca gac 612

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp

190 195 200

aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac 663

Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu Ser Ser Leu Ala Ser Glu Asp

205 210 215 220
 tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg 714
 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp
 225 230 235
 ggc caa ggc acc act ctc aca gtc tcc tca gac tac aaa gac gat gac gat 765
 Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp Tyr Lys Asp Asp Asp Asp
 240 245 250 255
 aaa taa tga gga tcc 780
 Lys

<210> 55
 <211> 351
 <212> DNA
 <213> Human
 <220>
 <221> CDS
 <222> (1)...(351)
 <223> 12B5HV. 1-351 peptide
 <400> 55

cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg tcc ctg agt ctc 60
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly Ser Leu Ser Leu
 5 10 15 20
 tcc tgt gca gtc tct gga atc acc ctc agg acc tac ggc atg cac tgg gtc cgc cag gct 120
 Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr Gly MET His Trp Val Arg Gln Ala
 25 30 35 40
 cca ggc aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga agt gaa tac tat 180
 Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg Ser Glu Tyr Tyr
 45 50 55 60
 gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt tcc aag aac acc ctg tat 240
 Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gcg aga gga gca 300
 Leu Gln MET Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ala

cat tat ggt ttc gat atc tgg ggc caa ggg aca atg gtc acc gtc tcg agt 351
 His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr MET Val Thr Val Ser Ser

<210> 56
 <211> 57
 <212> DNA
 <213> Human
 <220>
 <221> CDS
 <222> (1)...(57)
 <223> reader sequence
 <400> 56

atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga ggt gtc cag tgt 57
 MET Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly Val Gln Cys

5 10 15

<210> 57

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-1

<400> 57

atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60
 gtgcagctgg tgcagtctgg gggaggcttg gtccggcccc gggggtcctt gagtc 115

<210> 58

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-2

<400> 58

aaggatatac ctgccacca ctccagcccc ttgcctggag cctggcggac ccagtgcattg 60
 ccgtaggtcc tgagggtgat tccagagact gcacaggaga gactcaggga ccccc 115

<210> 59

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-3

<400> 59

ggcaggtata tcctttgacg gaagaagtga atactatgca gactccgtgc agggccgatt 60
 caccatctcc agagacagtt ccaagaacac cctgtatctg caaatgaaca gcctg 115

<210> 60

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-4

<400> 60

actcgagacg gtgaccattg tcccttggcc ccagatatcg aaaccataat gtgctcctct 60
 cgcacagtaa tacacagccg tgtcctcggc tctcaggctg ttcatttg 108

<210> 61

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-S, PCR primer

<400> 61

ttcaagcttc caccatggag ttgggctga gc 32

<210> 62

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-A, PCR primer

<400> 62

ttgggatcca ctcaccactc gagacgggtga ccat 34

<210> 63

<211> 433

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)...(419)

<223> HEF-12B5H-g gamma. 12-419 peptide

<400> 63

aagcttcac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga 56

MET Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg

1 5 10 15

ggt gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg 116

Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

20 25 30 35

tcc ctg agt ctc tcc tgt gca gtc tct gga atc acc ctc agg acc tac ggc atg cac tgg 176

Ser Leu Ser Leu Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr Gly MET His Trp

40 45 50 55

gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga 236

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg

60 65 70 75

agt gaa tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt tcc aag 296

Ser Glu Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys

80 85 90 95

aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 356

Asn Thr Leu Tyr Leu Gln MET Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

100 105 110 115

gcg aga gga gca cat tat ggt ttc gat atc tgg ggc caa ggg aca atg gtc acc gtc tcg 416

Ala Arg Gly Ala His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr MET Val Thr Val Ser

120 125 130 135

agt ggtgagtga tcc 433

Ser

<210> 64

<211> 323

<212> DNA

<213> Human

<220>

<221> CDS (

<222> (1)...(323)

<223> 12B5LV. 1-323 peptide

<400> 64

gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct att gga gac aga gtc acc 60
Asp Ile Gln MET Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr
5 10 15 20

atc acc tgc cgg gcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag aag cca 120
Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro

ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt tta gcc agt ggg gcc cca tca 180
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser

agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

gat gat ttg gca act tat tac tgc caa caa tat agt aat tat ccg ctc act ttc ggc gga 300
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly

ggg acc aag ctg gag atc aaa 323
Gly Thr Lys Leu Glu Ile Lys
105

<210> 65

<211> 66

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)...(57)

<223> reader sequence

<400> 65

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca ggt gcc 60
MET Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro Gly Ala

Aaa tgt 66
Lys Cys

<210> 66

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-1

<400> 66

atggacatga ggggtccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgcc 60
aaatgtgaca tccagatgac ccagtcctct tccaccctgt ctgcatctat 110

<210> 67

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-2

<400> 67

ggagtttagg ggctttccct ggcttctgct gataccaggc caaccagtga taaataccct 60
cgctggcccc gcaggtgatg gtgactctgt ctccaataga tgcagacagg 110

<210> 68

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-3

<400> 68

aagcccctaa actcctgatc tataaggcct ctagttagc cagtggggcc ccatcaaggt 60
tcagcggcag tggatctggg acagatttca ctctacccat cagcagcctg 110

<210> 69

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-4

<400> 69

accatcagca gcctgcagcc tgatgatttt gcaacttatt actgccaaca atatagtaat 60
tatccgctca ctttcggcgg agggaccaag ctggagatca aa 102

<210> 70

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-S, PCR primer

<400> 70

ttcaagcttc caccatggac atgagggatcc cc 32

<210> 71

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-A, PCR primer

<400> 71

tctaggatcc actcacgttt gatctccagc ttggt 35

<210> 72

<211> 415

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)...(398)

<223> HEF-12B5H-g kappa. 12-398 peptide

<400> 72

aagcttcac c atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc 56

MET Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu

1 5 10 15

tgg ctc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc ctg tct gca 116

Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln MET Thr Gln Ser Pro Ser Thr Leu Ser Ala

20 25 30 35

tct att gga gac aga gtc acc atc acc tgc cgg gcc agc gag ggt att tat cac tgg ttg 176

Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu

40 45 50 55

gcc tgg tat cag cag aag cca ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt 236

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser

60 65 70 75

tta gcc agt ggg gcc cca tca agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc 296

Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

80 85 90 95

acc atc agc agc ctg cag cct gat gat ttt gca act tat tac tgc caa caa tat agt aat 356

Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn

100 105 110 115

tat ccg ctc act ttc ggc gga ggg acc aag ctg gag atc aaa cgtgagtgga tcttaga 415

Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

120 125